

11420122.APP  
SEQUENCE LISTING

<110> Pausch, Mark H  
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011

<141> 1997-03-11

<150> 07/332,312

<151> 1994-10-31

<150> PCT/US95/14364

<151> 1995-10-25

<160> 67

<170> PatentIn Ver. 2.1

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Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly	245	250	255	
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Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr	275	280	285	
Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg	290	295	300	
Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr	305	310	315	320
Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp	325	330	335	
Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg	340	345	350	
Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly	355	360	365	
Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu	370	375	380	
Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu	385	390	395	400
Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu	405	410	415	
Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser	420	425	430	
Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr	435	440	445	
Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu				

450

455

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu  
465 470 475 480

Trp

<210> 38  
<211> 337  
<212> PRT  
<213> Caenorhabditis elegans

<220>  
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<222> (337)  
<223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

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20 25 30  
Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn  
35 40 45  
Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser  
50 55 60  
Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly  
65 70 75 80  
Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys  
85 90 95  
Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His  
100 105 110  
Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile  
115 120 125  
Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val  
130 135 140  
Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser  
145 150 155 160  
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly  
165 170 175  
Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu  
180 185 190  
Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe  
195 200 205  
Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val  
210 215 220  
Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln  
Page 13

225					230				235				240			
Asp	Ala	Arg	Ser	Ala	Leu	Ala	Val	Val	Gly	Gly	Lys	Val	Val	Leu	Val	
				245					250					255		
Ser	Glu	Leu	Tyr	Ala	Asn	Leu	Met	Gln	Lys	Arg	Ala	Arg	Asn	Met	Ser	
			260					265					270			
Arg	Glu	Ala	Phe	Ile	Val	Glu	Asn	Leu	Tyr	Val	Ser	Lys	His	Ile	Ile	
		275					280					285				
Pro	Phe	Ile	Pro	Thr	Asp	Ile	Arg	Cys	Ile	Arg	Tyr	Ile	Asp	Gln	Thr	
	290					295					300					
Ala	Asp	Ala	Ala	Thr	Ile	Ser	Thr	Ser	Ser	Ser	Ala	Ile	Asp	Met	Gln	
305					310					315					320	
Ser	Cys	Arg	Phe	Cys	His	Ser	Arg	Tyr	Ser	Leu	Asn	Arg	Ala	Phe	Lys	
				325					330					335		

Xaa

<210> 39  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
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PRIMER BASED ON HUMAN POTASSIUM CHANNELS

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<220>
<221> variation
<222> (2)
<223> N AT BASE 2 INDICATES ANY NUCLEOTIDE
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<400> 39	
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<210> 40  
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<212> DNA  
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PRIMER BASED ON HUMAN POTASSIUM CHANNELS

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<400> 40
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<210> 41
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<213> Homo sapiens
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<400> 41  
cgcaggcaga gccacaaaga gtacacag 28

<210> 42  
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 <212> DNA  
 <213> Homo sapiens

<400> 42  
 ggagatcagc taggcaccat atttgg 26

<210> 43  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
 atgctgcatg cctcatgctt cccagc 26

<210> 44  
 <211> 20  
 <212> DNA  
 <213> Homo sapiens

<400> 44  
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<210> 45  
 <211> 426  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
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 1 5 10 15

Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys  
 20 25 30

Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val  
 35 40 45

Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr  
 50 55 60

Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe  
 65 70 75 80

Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val  
 85 90 95

Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr  
 100 105 110

Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly  
 115 120 125

Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu  
 130 135 140

Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe  
 145 150 155 160

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Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile	Ile
				165					170					175	
Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	Gly	Val
			180					185					190		
Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val	Glu
		195					200					205			
Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	Ile	Ile
	210					215					220				
Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	Ala	Leu
	225				230					235					240
Pro	Ala	Ile	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	Asp	Ala
				245					250					255	
Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr
			260					265					270		
Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	Pro	Val
		275					280					285			
Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	Val	Leu
	290					295					300				
Ser	Met	Ile	Gly	Arg	Leu	Val	Arg	Val	Ile	Ser	Lys	Lys	Thr	Lys	Glu
	305				310					315					320
Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	Asn	Val
				325					330					335	
Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	Ile	Tyr
			340					345					350		
Asp	Lys	Phe	Gln	Arg	Ala	Thr	Ser	Ile	Lys	Arg	Lys	Leu	Ser	Ala	Glu
		355					360					365			
Leu	Ala	Gly	Asn	His	Asn	Gln	Glu	Leu	Thr	Pro	Cys	Arg	Arg	Thr	Leu
	370					375					380				
Ser	Val	Asn	His	Leu	Thr	Ser	Glu	Arg	Asp	Val	Leu	Pro	Pro	Leu	Leu
	385				390					395					400
Lys	Thr	Glu	Ser	Ile	Tyr	Leu	Asn	Gly	Leu	Ala	Pro	His	Cys	Ala	Gly
				405					410					415	
Glu	Glu	Ile	Ala	Val	Ile	Glu	Asn	Ile	Lys						
			420					425							

<210> 46  
 <211> 2130  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (35)  
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 NUCLEOTIDE



<220>  
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 <222> (2057)  
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<220>  
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 NUCLEOTIDE

<220>  
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 <222> (2111)  
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 NUCLEOTIDE

<220>  
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 <222> (2120)  
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 NUCLEOTIDE

<400> 46

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cgtgcagctc	gg	ggagcgcgca	gcccgtctct	gaataagaag	tgagtacaat	ggcgtgtttg	120
taaaaaaaag	ctt	caagtcc	gtctttttca	aaaaacattt	tgaatgctgc	atgcctcatg	180
cttcccagcg	cct	cgcggga	gagacccggc	tatagagcag	gagtggcggc	acctgacttg	240
ctggatccta	aat	ctgcccgc	tcagaactcc	aaaccgaggc	tctcattttc	cacgaaaccc	300
acagtgtctg	ctt	cccgggt	ggagagtgac	acgaccatta	atgttatgaa	atggaagacg	360
gtctccacga	tatt	ccttggg	ggttgcctc	tatctgatca	tcggagccac	cgtgttcaaa	420
gcattggagc	agc	ctcatga	gatttcacag	aggaccacca	ttgtgatcca	gaagcaaa	480
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aacatctcac	cac	gcacaga	aggcggcaaa	atattctgta	tcattctatgc	cttactggga	720
attcccctct	ttg	gttttct	cttggctgga	gttggagatc	agctaggcac	catatttgga	780
aaaggaattg	cca	aatgga	agatacgttt	attaagtggg	atgttagtca	gaccaagatt	840
cgcacatctc	caa	aatcat	atattatacta	tttggctgtg	tactctttgt	ggctctgcct	900
gcatcatat	tcaa	acacat	agaaggctgg	agtgccctgg	acgccattta	ttttgtgggt	960
atcactctaa	ca	actattgg	atattgggtgac	tacgttgacg	gtggatccga	tattgaatat	1020
ctggacttct	ata	agcctgt	cgtgtgggtc	tggatccttg	tagggcttgc	ttactttgct	1080
gctgtcctga	gc	atgattgg	gagattgggtc	cgagtgatat	ctaaaaagac	aaaagaagag	1140
gtgggagagt	tc	agagcaca	cgctgctgag	tggacagcca	acgtcacagc	cgaattcaaa	1200
gaaaccagga	gg	cgcactgag	tgtggagatt	tatgacaagt	tccagcgggc	cacctccatc	1260
aagcgggaagc	tct	cggcaga	actggctgga	aaccacaatc	aggagctgac	tccttgtagg	1320
aggaccctgt	cag	tgaacca	cctgaccagc	gagagggatg	tcttgccctc	cttactgaag	1380
actgagagta	tct	atctgaa	tggtttggtg	ccacactgtg	ctggtgaaga	gattgctgtg	1440
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gagccagcac	ttt	ctttctg	atgatgcttg	ttgaacggcc	cactttcttt	gatgagtggg	1680
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atcttctgtca	gt	gccttatc	ttatgaagaa	acagaacctc	tctagcta	at	1980
tccttccctg	cccc	acccc	taggctcacc	tctgcagtct	tttaccctag	ttctccatt	2040
tgaataccat	ac	cttgnrtgg	aaacagngtg	taaaatgact	gaagtgatga	tgccgaagat	2100
gaaatagatg	ncaa	attagn	tggacattga				2130

<210> 47  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 aaaagatcta aaatgcttcc cagcgcc

27

<210> 48  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 aaagtcgacc tatttgatgt tctcaat

27

<210> 49  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 aaaaagctta aaatgcttcc cagcgcc

27

<210> 50  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 50  
 aaatctagac tatttgatgt tctcaat

27

<210> 51  
 <211> 534  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (262)  
 <223> N AT POSITION 262 INDICATES UNDETERMINED  
 NUCLEOTIDE

<400> 51  
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 gagcagagcc agctagaacc tgggcctggc cagttcaagg ccaccagagg gcagccttct 120  
 gcggaaggca gtattgggggt aggcagggac cccagcagac atggcactca gagctctcac 180  
 tgtccactga ctctctcttc tccaggttat ggccacatgg cccactatc gccaggcgga 240  
 aaggccttct gcatggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300  
 accctgcgcc attgcctgct gcctgtgctc agccgcccac gtgcctgggt agcgggtccac 360  
 tggcagctgt caccggccag ggctgcgctg ctgcaggcag ttgactggg actgctggtg 420  
 gccagcagct ttgtgctgct gccagcgctg gtgctgtggg gccttcaggg cgactgcagc 480  
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<210> 52  
 <211> 956  
 <212> DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 52

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acgaggagaa	tgtgcgcac	ttggctctca	tcgtgtgcac	cttcacctac	ctgctgggtg	120
gcgccgcggt	gttcgacgca	ctggagtcgg	agccggagat	gatcgagcgg	cagcggctgg	180
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tggagcgcgt	cgtgctgcgc	ctcaagccgc	acaaggccgg	cgtgcagtgg	cgcttcgccg	300
gctccttcta	cttcgccatc	accgtcatca	ccaccatcgg	ctatggtcac	gcggcgccca	360
gcacggacgg	aggcaagggt	ttctgcatgt	tctacgcgct	gctgggcatc	ccgctcacac	420
tagtcatggt	ccagagcctg	ggtgaacgca	tcaacacctc	cgtgaggtac	ctgctgcacc	480
gtgccaaag	ggggctgggc	atgcggcacg	ccgaagtgtc	catggccaac	atggtgctca	540
tcggtttcgt	gtcgtgcac	agcacgctgt	gcacgcggcg	agctgccttc	tcctactacg	600
agcgtcggac	tttcttccag	gcctattact	actgcttcat	caccctcacc	accatcggct	660
tcggcgacta	tgtggcgctg	cagaaggacc	aggcgctgca	gacgcagccg	cagtatgtgg	720
cttcagcttc	gtgtacatcc	tcacgggctc	acggtcacgc	gcgcttcctc	aacctcgtgg	780
tgctgcgatt	catgaccatg	aacgcccagg	acgagaagcg	tgatgcggag	caccgcgccc	840
tgctcacgca	caacggccag	gctgtcggcc	tgggtggcct	gagctgcctg	agcggtagcc	900
tgggcgacgg	cgtgcgtccc	cgcgaccagg	tcacatgcgc	tgcggccgca	agctta	956

&lt;210&gt; 53

&lt;211&gt; 1055

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (247)

&lt;223&gt; N AT POSITION 247 INDICATES UNDETERMINED NUCLEOTIDE

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (593)

&lt;223&gt; N AT POSITION 593 INDICATES UNDETERMINED NUCLEOTIDE

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (952)

&lt;223&gt; N AT POSITION 952 INDICATES UNDETERMINED NUCLEOTIDE

&lt;400&gt; 53

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ggggctgtgg	tgcttcaggc	cctggagggc	cctccagctc	gccacctcca	ggcccagggtc	120
caggctgaac	tggctagctt	ccaggcagag	cacagggcct	gcttgccacc	tgaggccctg	180
gaggagctgc	taggtgcggt	cctgagagca	caggcccatg	gagtttccag	cctgggcaac	240
agctcanaga	caagcaactg	ggatctgccc	tcagctctgc	tgttcactgc	cagcatcctc	300
accaccaccg	gttatggcca	catggcccca	ctctcctcag	gtggaaaggc	cttctgtgtg	360
gtctatgcag	cccttgggct	gccagcctct	ctagcacttg	tggctgccct	gcgccactgc	420
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gctcaggctg	ctctgctaca	ggcagcagga	ctgggcctcc	tgggtggcctg	tgtcttcatg	540
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tacttctgtt	tcggctcact	cagcacgata	ggcctaggag	acttgctgcc	tgcccattgga	660
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gccatggtga	aattcttttg	gcccagtggc	tctagaaccg	atgaagatca	agatggcatc	840
ctaggccaag	atgagctggc	tctgagcact	gtgctgcctg	acgccccagt	cttgggacca	900
accacccag	cctgagcggg	aggcaccaag	gagtgcttga	agaacatagc	angaagggtt	960
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tgcaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaa			1055

<210> 54  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (88)  
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 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly  
 35 40 45  
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr  
 50 55 60  
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
 65 70 75 80  
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
 85 90 95  
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
 100 105 110  
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
 115 120 125  
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
 130 135 140  
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
 145 150 155 160  
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
 165 170 175  
 Leu Gly

<210> 55  
 <211> 309  
 <212> PRT  
 <213> Mus musculus

<400> 55  
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 20 25 30  
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln

35 40 45  
 Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
     50                      55                      60  
 Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
     65                      70                      75                      80  
 His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala  
                                     85                      90                      95  
 Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
                                     100                      105                      110  
 Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
                                     115                      120                      125  
 Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
                                     130                      135                      140  
 Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
     145                      150                      155                      160  
 Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
                                     165                      170                      175  
 Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg  
                                     180                      185                      190  
 Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
                                     195                      200                      205  
 Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
                                     210                      215                      220  
 Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala  
     225                      230                      235                      240  
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr  
                                     245                      250                      255  
 Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu  
                                     260                      265                      270  
 Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser  
                                     275                      280                      285  
 Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala  
     290                      295                      300  
 Ala Ala Ala Ser Leu  
 305

&lt;210&gt; 56

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (83)

&lt;223&gt; N AT POSITION 83 INDICATES UNDETERMINED RESIDUE

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (198)

&lt;223&gt; N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

&lt;400&gt; 56

Leu	Lys	Pro	Trp	Ala	Arg	Tyr	Leu	Leu	Leu	Leu	Met	Ala	His	Leu	Leu
1				5				10						15	
Ala	Met	Gly	Leu	Gly	Ala	Val	Val	Leu	Gln	Ala	Leu	Glu	Gly	Pro	Pro
			20					25					30		
Ala	Arg	His	Leu	Gln	Ala	Gln	Val	Gln	Ala	Glu	Leu	Ala	Ser	Phe	Gln
		35					40					45			
Ala	Glu	His	Arg	Ala	Cys	Leu	Pro	Pro	Glu	Ala	Leu	Glu	Glu	Leu	Leu
	50					55					60				
Gly	Ala	Val	Leu	Arg	Ala	Gln	Ala	His	Gly	Val	Ser	Ser	Leu	Gly	Asn
65					70					75					80
Ser	Ser	Xaa	Thr	Ser	Asn	Trp	Asp	Leu	Pro	Ser	Ala	Leu	Leu	Phe	Thr
				85					90					95	
Ala	Ser	Ile	Leu	Thr	Thr	Thr	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser
			100					105					110		
Ser	Gly	Gly	Lys	Ala	Phe	Cys	Val	Val	Tyr	Ala	Ala	Leu	Gly	Leu	Pro
		115					120					125			
Ala	Ser	Leu	Ala	Leu	Val	Ala	Ala	Leu	Arg	His	Cys	Leu	Leu	Pro	Val
	130					135					140				
Phe	Ser	Arg	Pro	Gly	Asp	Trp	Val	Ala	Ile	Arg	Trp	Gln	Leu	Ala	Pro
145					150					155					160
Ala	Gln	Ala	Ala	Leu	Leu	Gln	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Val	Ala
				165					170					175	
Cys	Val	Phe	Met	Leu	Leu	Pro	Ala	Leu	Val	Leu	Trp	Gly	Val	Gln	Gly
			180					185					190		
Asp	Trp	Gln	Pro	Ala	Xaa	Thr	Ile	Tyr	Phe	Cys	Phe	Gly	Ser	Leu	Ser
		195					200					205			
Thr	Ile	Gly	Leu	Gly	Asp	Leu	Leu	Pro	Ala	His	Gly	Arg	Gly	Leu	His
	210					215					220				
Pro	Ala	Ile	Tyr	His	Leu	Gly	Gln	Phe	Ala	Leu	Leu	Gly	Tyr	Leu	Leu
225					230					235					240
Leu	Gly	Leu	Leu	Ala	Met	Leu	Leu	Ala	Val	Glu	Thr	Phe	Ser	Glu	Leu
				245					250					255	
Pro	Gln	Val	Arg	Ala	Met	Val	Lys	Phe	Phe	Gly	Pro	Ser	Gly	Ser	Arg
			260					265					270		
Thr	Asp	Glu	Asp	Gln	Asp	Gly	Ile	Leu	Gly	Gln	Asp	Glu	Leu	Ala	Leu
		275					280					285			
Ser	Thr	Val	Leu	Pro	Asp	Ala	Pro	Val	Leu	Gly	Pro	Thr	Thr	Pro	Ala
	290					295					300				

<210> 57  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <221> VARIANT  
 <222> (1)..(9)  
 <223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT  
 POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8  
 IS Y, F, V, I, M, OR L  
  
 <220>  
 <223> Description of Artificial Sequence: POTASSIUM ION  
 CHANNEL SEQUENCE  
  
 <400> 57  
 Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly  
 1 5  
  
 <210> 58  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: POTASSIUM ION  
 CHANNEL SEQUENCE  
  
 <220>  
 <221> VARIANT  
 <222> (1)..(8)  
 <223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,  
 S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I,  
 V, L, F, OR Y  
  
 <400> 58  
 Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa  
 1 5  
  
 <210> 59  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: POTASSIUM ION  
 CHANNEL SEQUENCE  
  
 <400> 59  
 Tyr Ala Leu Leu Gly Ile Pro  
 1 5  
  
 <210> 60  
 <211> 7

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: POTASSIUM ION  
 CHANNEL SEQUENCE

<220>  
 <221> VARIANT  
 <222> (6)  
 <223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60  
 Tyr Ala Leu Leu Gly Xaa Pro  
 1 5

<210> 61  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (88)  
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61  
 Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser  
 1 5 10 15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe  
 20 25 30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly  
 35 40 45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr  
 50 55 60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
 65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
 85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
 100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
 115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
 130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
 145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
 165 170 175

Leu Gly



<210> 62  
 <211> 309  
 <212> PRT  
 <213> Mus musculus

<400> 62

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg  
 1 5 10 15  
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala  
 20 25 30  
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln  
 35 40 45  
 Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
 50 55 60  
 Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
 65 70 75 80  
 His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala  
 85 90 95  
 Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
 100 105 110  
 Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
 115 120 125  
 Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
 130 135 140  
 Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
 145 150 155 160  
 Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
 165 170 175  
 Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg  
 180 185 190  
 Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
 195 200 205  
 Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
 210 215 220  
 Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala  
 225 230 235 240  
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr  
 245 250 255  
 Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu  
 260 265 270  
 Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser  
 275 280 285  
 Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala

290

295

Ala Ala Ala Ser Leu  
305

<210> 63  
<211> 434  
<212> PRT  
<213> Caenorhabditis elegans

<400> 63  
Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala  
1 5 10 15  
Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val  
20 25 30  
Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro  
35 40 45  
Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp  
50 55 60  
Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro  
65 70 75 80  
Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro  
85 90 95  
Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu  
100 105 110  
Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser  
115 120 125  
Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn  
130 135 140  
Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp  
145 150 155 160  
Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys  
165 170 175  
Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn  
180 185 190  
Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val  
195 200 205  
Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp  
210 215 220  
Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala  
225 230 235 240  
Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn  
245 250 255  
Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu  
260 265 270

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Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly  
275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu  
290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val  
305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile  
325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn Tyr Arg  
340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe  
355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala  
370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg  
385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr  
405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser  
420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,  
S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,  
L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro  
1 5

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence between Ce orf1 and Dm orf1

<400> 65  
Thr Trp Thr Phe  
1

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<210> 66  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence between Ce orf1 and Dm orf1

<400> 66  
Gly Tyr Gly Asn  
1

<210> 67  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence between Ce orf1 and Dm orf1

<400> 67  
Gly Phe Gly Asp  
1